

RAW SEQUENCE LISTING

re-run

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/585,841
Source: two
Date Processed by STIC: 7/20/06

ENTERED



RAW SEQUENCE LISTING

DATE: 09/02/2008

PATENT APPLICATION: US/10/585,841

TIME: 14:24:17

Input Set : E:\211010053P1.SEQ.TXT

Output Set: N:\CRF4\09022008\J585841.raw

4 <110> APPLICANT: University of Utah Research Foundation
 6 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
 7 DHR96
 9 <130> FILE REFERENCE: 21101.0053P1
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/585,841
 C--> 12 <141> CURRENT FILING DATE: 2006-07-12
 14 <150> PRIOR APPLICATION NUMBER: 60/536,337
 15 <151> PRIOR FILING DATE: 2004-01-13
 17 <160> NUMBER OF SEQ ID NOS: 60
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1543
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Artificial Sequence
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
 28 synthetic construct
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 32 1 5 10 15
 33 Phe Gln Asp Leu Lys Leu Lys Arg Arg Lys Ile Asp Ser Arg Cys Ser
 34 20 25 30
 35 Ser Asp Gly Glu Ser Ile Ala Asp Thr Ser Thr Ser Ser Pro Asp Leu
 36 35 40 45
 37 Leu Ala Pro Met Ser Pro Lys Leu Cys Asp Ser Gly Ser Ala Gly Ala
 38 50 55 60
 39 Ser Leu Gly Ala Ser Leu Pro Leu Pro Leu Ala Leu Pro Leu Pro Met
 40 65 70 75 80
 41 Ala Leu Pro Leu Pro Met Ser Leu Pro Leu Pro Leu Thr Ala Ala Ser
 42 85 90 95
 43 Ser Ala Val Thr Val Ser Leu Ala Ala Val Val Ala Ala Val Ala Glu
 44 100 105 110
 45 Thr Gly Gly Ala Gly Ala Gly Gly Ala Gly Thr Ala Val Thr Ala Ser
 46 115 120 125
 47 Gly Ala Gly Pro Cys Val Ser Thr Ser Ser Thr Thr Ala Ala Ala Ala
 48 130 135 140
 49 Thr Ser Ser Thr Ser Ser Leu Ser Ser Ser Ser Ser Ser Ser Ser
 50 145 150 155 160
 51 Thr Ser Ser Ser Thr Ser Ser Ala Ser Pro Thr Ala Gly Ala Ser Ser
 52 165 170 175
 53 Thr Ala Thr Cys Pro Ala Ser Ser Ser Ser Ser Ser Gly Asn Gly Ser
 54 180 185 190
 55 Gly Gly Lys Ser Gly Ser Ile Lys Gln Glu His Thr Glu Ile His Ser

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56          195          200          205
57 Ser Ser Ser Ala Ile Ser Ala Ala Ala Ala Ser Thr Val Met Ser Pro
58      210          215          220
59 Pro Pro Ala Glu Ala Thr Arg Ser Ser Pro Ala Thr Pro Glu Gly Gly
60 225          230          235          240
61 Gly Pro Ala Gly Asp Gly Ser Gly Ala Thr Gly Gly Gly Asn Thr Ser
62          245          250          255
63 Gly Gly Ser Thr Ala Gly Val Ala Ile Asn Glu His Gln Asn Asn Gly
64          260          265          270
65 Asn Gly Ser Gly Gly Ser Ser Arg Ala Ser Pro Asp Ser Leu Glu Glu
66      275          280          285
67 Lys Pro Ser Thr Thr Thr Thr Thr Gly Arg Pro Thr Leu Thr Pro Thr
68      290          295          300
69 Asn Gly Val Leu Ser Ser Ala Ser Ala Gly Thr Gly Ile Ser Thr Gly
70 305          310          315          320
71 Ser Ser Ala Lys Leu Ser Glu Ala Gly Met Ser Val Ile Arg Ser Val
72          325          330          335
73 Lys Glu Glu Arg Leu Leu Asn Val Ser Ser Lys Met Leu Val Phe His
74          340          345          350
75 Gln Gln Arg Glu Gln Glu Thr Lys Ala Val Ala Ala Ala Ala Ala Ala
76          355          360          365
77 Ala Ala Ala Gly His Val Thr Val Leu Val Thr Pro Ser Arg Ile Lys
78      370          375          380
79 Ser Glu Pro Pro Pro Pro Ala Ser Pro Ser Ser Thr Ser Ser Thr Gln
80 385          390          395          400
81 Arg Glu Arg Glu Arg Glu Arg Asp Arg Glu Arg Asp Arg Glu Arg Glu
82          405          410          415
83 Arg Glu Arg Asp Arg Asp Arg Glu Arg Glu Arg Glu Gln Ser Ile Ser
84          420          425          430
85 Ser Ser Gln Gln His Leu Ser Arg Val Ser Ala Ser Pro Pro Thr Gln
86      435          440          445
87 Leu Ser His Gly Ser Leu Gly Pro Asn Ile Val Gln Thr His His Leu
88      450          455          460
89 His Gln Gln Leu Thr Gln Pro Leu Thr Leu Arg Lys Ser Ser Pro Pro
90 465          470          475          480
91 Thr Glu His Leu Leu Ser Gln Ser Met Gln His Leu Thr Gln Gln Gln
92          485          490          495
93 Ala Ile His Leu His His Leu Leu Gly Gln Gln Gln Gln Gln Gln Gln
94          500          505          510
95 Ala Ser His Pro Gln Gln Gln Gln Gln Gln Gln His Ser Pro His Ser
96          515          520          525
97 Leu Val Arg Val Lys Lys Glu Pro Asn Val Gly Gln Arg His Leu Ser
98      530          535          540
99 Pro His His Gln Gln Gln Ser Pro Leu Leu Gln His His Gln Gln Gln
100 545          550          555          560
101 Gln Gln Gln Gln Gln Gln Gln Gln Gln His Leu His Gln Gln Gln Gln
102          565          570          575
103 Gln Gln Gln His His Gln Gln Gln Pro Gln Ala Leu Ala Leu Met His
104          580          585          590

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105 Pro Ala Ser Leu Ala Leu Arg Asn Ser Asn Arg Asp Ala Ala Ile Leu
106      595      600      605
107 Phe Arg Val Lys Ser Glu Val His Gln Gln Val Ala Ala Gly Leu Pro
108      610      615      620
109 His Leu Met Gln Ser Ala Gly Gly Ala Ala Ala Ala Ala Ala Ala
110 625      630      635      640
111 Val Ala Ala Gln Arg Met Val Cys Phe Ser Asn Ala Arg Ile Asn Gly
112      645      650      655
113 Val Lys Pro Glu Val Ile Gly Gly Pro Leu Gly Asn Leu Arg Pro Val
114      660      665      670
115 Gly Val Gly Gly Gly Asn Gly Ser Gly Ser Val Gln Cys Pro Ser Pro
116      675      680      685
117 His Pro Ser Ser Ser Ser Ser Ser Ser Gln Leu Ser Pro Gln Thr Pro
118      690      695      700
119 Ser Gln Thr Pro Pro Arg Gly Thr Pro Thr Val Ile Met Gly Glu Ser
120 705      710      715      720
121 Cys Gly Val Arg Thr Met Val Trp Gly Tyr Glu Pro Pro Pro Pro Ser
122      725      730      735
123 Ala Gly Gln Ser His Gly Gln His Pro Gln Gln Gln Gln Gln Ser Pro
124      740      745      750
125 His His Gln Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Gln
126      755      760      765
127 Gln Gln Gln Gln Gln Gln Gln Gln Gln Ser Leu Gly Gln Gln Gln His
128      770      775      780
129 Cys Leu Ser Ser Pro Ser Ala Gly Ser Leu Thr Pro Ser Ser Ser Ser
130 785      790      795      800
131 Gly Gly Gly Ser Val Ser Gly Gly Gly Val Gly Gly Pro Leu Thr Pro
132      805      810      815
133 Ser Ser Val Ala Pro Gln Asn Asn Glu Glu Ala Ala Gln Leu Leu Leu
134      820      825      830
135 Ser Leu Gly Gln Thr Arg Ile Gln Asp Met Arg Ser Arg Pro His Pro
136      835      840      845
137 Phe Arg Thr Pro His Ala Leu Asn Met Glu Arg Leu Trp Ala Gly Asp
138      850      855      860
139 Tyr Ser Gln Leu Pro Pro Gly Gln Leu Gln Ala Leu Asn Leu Ser Ala
140 865      870      875      880
141 Gln Gln Gln Gln Trp Gly Ser Ser Asn Ser Thr Gly Leu Gly Gly Val
142      885      890      895
143 Gly Gly Gly Met Gly Gly Arg Asn Leu Glu Ala Pro His Glu Pro Thr
144      900      905      910
145 Asp Glu Asp Glu Gln Pro Leu Val Cys Met Ile Cys Glu Asp Lys Ala
146      915      920      925
147 Thr Gly Leu His Tyr Gly Ile Ile Thr Cys Glu Gly Cys Lys Gly Phe
148      930      935      940
149 Phe Lys Arg Thr Val Gln Asn Arg Arg Val Tyr Thr Cys Val Ala Asp
150 945      950      955      960
151 Gly Thr Cys Glu Ile Thr Lys Ala Gln Arg Asn Arg Cys Gln Tyr Cys
152      965      970      975
153 Arg Phe Lys Lys Cys Ile Glu Gln Gly Met Val Leu Gln Ala Val Arg

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154          980          985          990
155 Glu Asp Arg Met Pro Gly Gly Arg Asn Ser Gly Ala Val Tyr Asn Leu
156          995          1000          1005
157 Tyr Lys Val Lys Tyr Lys Lys His Lys Lys Thr Asn Gln Lys Gln Gln
158          1010          1015          1020
159 Gln Gln Ala Ala Gln Gln Gln Gln Gln Gln Ala Ala Ala Gln Gln Gln
160 1025          1030          1035          1040
161 His Gln Gln Gln Gln Gln His Gln Gln His Gln Gln His Gln Gln Gln
162          1045          1050          1055
163 Gln Leu His Ser Pro Leu His His His His His Gln Gly His Gln Ser
164          1060          1065          1070
165 His His Ala Gln Gln Gln His His Pro Gln Leu Ser Pro His His Leu
166          1075          1080          1085
167 Leu Ser Pro Gln Gln Gln Gln Gln Leu Ala Ala Ala Val Ala Ala Ala Ala
168          1090          1095          1100
169 Gln His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala
170 1105          1110          1115          1120
171 Lys Leu Met Gly Gly Val Val Asp Met Lys Pro Met Phe Leu Gly Pro
172          1125          1130          1135
173 Ala Leu Lys Pro Glu Leu Leu Gln Ala Pro Pro Met His Ser Pro Ala
174          1140          1145          1150
175 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Ser
176          1155          1160          1165
177 Pro His Leu Ser Leu Ser Ser Pro His Gln Gln Gln Gln Gln Gln Gln
178          1170          1175          1180
179 Gly Gln His Gln Asn His His Gln Gln Gln Gly Gly Gly Gly Gly Gly
180 1185          1190          1195          1200
181 Ala Gly Gly Gly Ala Gln Leu Pro Pro His Leu Val Asn Gly Thr Ile
182          1205          1210          1215
183 Leu Lys Thr Ala Leu Thr Asn Pro Ser Glu Ile Val His Leu Arg His
184          1220          1225          1230
185 Arg Leu Asp Ser Ala Val Ser Ser Ser Lys Asp Arg Gln Ile Ser Tyr
186          1235          1240          1245
187 Glu His Ala Leu Gly Met Ile Gln Thr Leu Ile Asp Cys Asp Ala Met
188          1250          1255          1260
189 Glu Asp Ile Ala Thr Leu Pro His Phe Ser Glu Phe Leu Glu Asp Lys
190 1265          1270          1275          1280
191 Ser Glu Ile Ser Glu Lys Leu Cys Asn Ile Gly Asp Ser Ile Val His
192          1285          1290          1295
193 Lys Leu Val Ser Trp Thr Lys Lys Leu Pro Phe Tyr Leu Glu Ile Pro
194          1300          1305          1310
195 Val Glu Ile His Thr Lys Leu Leu Thr Asp Lys Trp His Glu Ile Leu
196          1315          1320          1325
197 Ile Leu Thr Thr Ala Ala Tyr Gln Ala Leu His Gly Lys Arg Arg Gly
198          1330          1335          1340
199 Glu Gly Gly Gly Ser Arg His Gly Ser Pro Ala Ser Thr Pro Leu Ser
200 1345          1350          1355          1360
201 Thr Pro Thr Gly Thr Pro Leu Ser Thr Pro Ile Pro Ser Pro Ala Gln
202          1365          1370          1375

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203 Pro Leu His Lys Asp Asp Pro Glu Phe Val Ser Glu Val Asn Ser His
204           1380           1385           1390
205 Leu Ser Thr Leu Gln Thr Cys Leu Thr Thr Leu Met Gly Gln Pro Ile
206           1395           1400           1405
207 Ala Met Glu Gln Leu Lys Leu Asp Val Gly His Met Val Asp Lys Met
208           1410           1415           1420
209 Thr Gln Ile Thr Ile Met Phe Arg Arg Ile Lys Leu Lys Met Glu Glu
210 1425           1430           1435           1440
211 Tyr Val Cys Leu Lys Val Tyr Ile Leu Leu Asn Lys Gly Thr Trp Phe
212           1445           1450           1455
213 Asp Leu Gln Asn Pro Phe Ile Gln Cys Ser Cys Tyr Leu Leu Val Arg
214           1460           1465           1470
215 Phe Val Asn Pro Ala Glu Val Glu Leu Glu Ser Ile Gln Glu Arg Tyr
216           1475           1480           1485
217 Val Gln Val Leu Arg Ser Tyr Leu Gln Asn Ser Ser Pro Gln Asn Pro
218           1490           1495           1500
219 Gln Ala Arg Leu Ser Glu Leu Leu Ser His Ile Pro Glu Ile Gln Ala
220 1505           1510           1515           1520
221 Ala Ala Ser Leu Leu Leu Glu Ser Lys Met Phe Tyr Val Pro Phe Val
222           1525           1530           1535
223 Leu Asn Ser Ala Ser Ile Arg
224           1540
226 <210> SEQ ID NO: 2
227 <211> LENGTH: 4632
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
233     synthetic construct
235 <400> SEQUENCE: 2
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237 aaactcaaac ggcgcaaaat cgattcgcga tgcagcagtg acggcgagtc catagcggac      120
238 acgtccacac cgtcgccgga cctgctggcg cccatgtcgc cgaagctctg cgacagcggc      180
239 tcggcggggg cgtcgctggg ggcacgcgtg cccctgccgc tggccctgcc cctgccaatg      240
240 gccctgccac tgcccattgc gctgcccctg cccctcacgg cggcatcttc ggcggtcacc      300
241 gtttcgctgg cagcggctgt ggccgcggtg gccgagacgg gtggcgcggg cgcgggagga      360
242 gctgggacag cagtaacagc gtcgggagca ggaccatgcg tctccacgtc gtctacgacg      420
243 gcagcggcag ccacatcttc gacctctctg ctctcgtcct cctcctcttc gtcactctcc      480
244 acgtcctcca gcaattcttc cgctcgcgag acagctggag cctcctccac ggccacctgc      540
245 cccgccagca gcagcagcag cagtggaaac ggaagtgggg gcaaaagtgg tagcatcaag      600
246 caggagcaca cggagataca ctcgtcgagc agtgcgattt cggcgggcgc cgctcaacg      660
247 gtgatgtcac cgccgcccgc tgaggcgacg agatccagtc cagccacgcc cgagggaggg      720
248 ggaccagctg gcgacggaag tggagcaacg ggaggcgga aacacgagcg cggatcaacg      780
249 gctggagtgg ccattaatga acacaaaac aatggcaatg gcagcggcgg gagcagtcga      840
250 gcctctcccg attcgctgga agagaagccc tctaccacaa cgaccacagg tcgtccaacg      900
251 ctacgcccga cgaatgggtg gctgtcctcc gcctcggcgg gcacggggat ttccacagga      960
252 agcagcgcca agctgagcga ggctggatat agtgtgatac ggtccgtgaa ggaggagcgc      1020
253 ttgctcaacg tatccagcaa gatgctggtg ttccatcagc agcgggagca agagacccaa      1080
254 gcagtggcgg ctgcagcagc agcagcagcg gcgggccatg tgacggttct agtgacgcca      1140

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/585,841

DATE: 09/02/2008

TIME: 14:24:18

Input Set : E:\211010053P1.SEQ.TXT

Output Set: N:\CRF4\09022008\J585841.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date